PCT09

RAW SEQUENCE LISTING DATE: 01/14/2002
PATENT APPLICATION: US/09/889,314 TIME: 13:39:58

Input Set : A:\1990035b.app
Output Set: N:\CRF3\01142002\I889314.raw

Does Not Comply
Corrected Diskette Needed

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  3 <110> APPLICANT: BURNIE, JAMES PETER
  4       MATTHEWS, RUTH CHRISTINE
  6 <120> TITLE OF INVENTION: MEDICAMENT
  8 <130> FILE REFERENCE: 050885-0281578
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/889,314
C--> 11 <141> CURRENT FILING DATE: 2001-11-20
W--> 13 <140> CURRENT APPLICATION NUMBER: GB 9902555.3
C--> 14 <141> CURRENT FILING DATE: 1999-02-05
 16 <150> PRIOR APPLICATION NUMBER: 09/889,314
 17 <151> PRIOR FILING DATE: 2001-07-16
 19 <160> NUMBER OF SEQ ID NOS: 16
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1491
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Chlamydia pneumoniae
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)..(1491)
 32 <400> SEQUENCE: 1
 33 gat aca aac atg tct att tca tct tct tca gga cct gac aat caa aaa   48
 34 Asp Thr Asn Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys
 35   1               5                  10                  15
 37 aat atc atg tct caa gtt ctg aca tcg aca ccc cag ggc gtg ccc caa   96
 38 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln
 39              20                  25                  30
 41 caa gat aag ctg tct ggc aac gaa acg aag caa ata cag caa aca cgt   144
 42 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg
 43          35                  40                  45
 45 cag ggt aaa aac act gag atg gaa agc gat gcc act att gct ggt gct   192
 46 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala
 47      50                  55                  60
 49 tct gga aaa gac aaa act tcc tcg act aca aaa aca gaa aca gct cca   240
 50 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro
 51  65                  70                  75                  80
 53 caa cag gga gtt gct gct ggg aaa gaa tcc tca gaa agt caa aag gca   288
 54 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala
 55                  85                  90                  95
 57 ggt gct gat act gga gta tca gga gcg gct gct act aca gca tca aat   336
 58 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn
 59              100                 105                 110
 61 act gca aca aaa att gct atg cag acc tct att gaa gag gcg agc aaa   384
 62 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys
 63          115                 120                 125
 65 agt atg gag tct acc tta gag tca ctt caa agc ctc agt gcc gcg caa   432
 66 Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln
 67      130                 135                 140
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69 atg aaa gaa gtc gaa gcg gtt gtt gtt gct gcc ctc tca ggg aaa agt   480
70 Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser
71 145                 150                 155                 160
73 tcg ggt tcc gca aaa ttg gaa aca cct gag ctc ccc aag ccc ggg gtg   528
74 Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val
75                  165                 170                 175
77 aca cca aga tca gag gtt atc gaa atc gga ctc gcg ctt gct aaa gca   576
78 Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala
79              180                 185                 190
81 att cag aca ttg gga gaa gcc aca aaa tct gcc tta tct aac tat gca   624
82 Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala
83          195                 200                 205
85 agt aca caa gca caa gca gac caa aca aat aaa cta ggt cta gaa aag   672
86 Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys
87      210                 215                 220
89 caa gcg ata aaa atc gat aaa gaa cga gaa gaa tac caa gag atg aag   720
90 Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys
91 225                 230                 235                 240
93 gct gcc gaa cag aag tct aaa gat ctc gaa gga aca atg gat act gtc   768
94 Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val
95                  245                 250                 255
97 aat act gtg atg atc gcg gtt tct gtt gcc att aca gtt att tct att   816
98 Asn Thr Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile
99              260                 265                 270
101 gtt gct gct att ttt aca tgc gga gct gga ctc gct gga ctc gct gcg   864
102 Val Ala Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala
103         275                 280                 285
105 gga gct gct gta ggt gca gcg gca gct gga ggt gca gca gga gct gct   912
106 Gly Ala Ala Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala
107     290                 295                 300
109 gcc gca acc acg gta gca aca caa att aca gtt caa gct gtt gtc caa   960
110 Ala Ala Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln
111 305                 310                 315                 320
113 gcg gtg aaa caa gct gtt atc aca gct gtc aga caa gcg atc acc gcg   1008
114 Ala Val Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala
115                 325                 330                 335
117 gct ata aaa gcg gct gtc aaa tct gga ata aaa gca ttt atc aaa act   1056
118 Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr
119             340                 345                 350
121 tta gtc aaa gcg att gcc aaa gcc att tct aaa gga atc tct aag gtt   1104
122 Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val
123         355                 360                 365
125 ttc gct aag gga act caa atg att gcg aag aac ttc ccc aag ctc tcg   1152
126 Phe Ala Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser
127     370                 375                 380
129 aaa gtc atc tcg tct ctt acc agt aaa tgg gtc acg gtt ggg gtt ggg   1200
130 Lys Val Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly
131 385                 390                 395                 400
133 gtt gta gtt gcg gcg cct gct ctc ggt aaa ggg att atg caa atg cag   1248
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```
134 Val Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln
135                 405                 410                 415
137 ctc tcg gag atg caa caa aac gtc gct caa ttt cag aaa gaa gtc gga   1296
138 Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly
139             420                 425                 430
141 aaa ctg cag gct gcg gct gat atg att tct atg ttc act caa ttt tgg   1344
142 Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp
143         435                 440                 445
145 caa cag gca agt aaa att gcc tca aaa caa aca ggc gag tct aat gaa   1392
146 Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu
147     450                 455                 460
149 atg act caa aaa gct acc aag ctg ggc gct caa atc ctt aaa gcg tat   1440
150 Met Thr Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr
151 465                 470                 475                 480
153 gcc gca atc agc gga gcc atc gct ggc gca cat aaa acc aat aat ttt   1488
154 Ala Ala Ile Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe
155                 485                 490                 495
157 taa                                                           1491
161 <210> SEQ ID NO: 2
162 <211> LENGTH: 496
163 <212> TYPE: PRT
164 <213> ORGANISM: Chlamydia pneumoniae
166 <400> SEQUENCE: 2
167 Asp Thr Asn Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys
168   1               5                  10                  15
170 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln
171             20                  25                  30
173 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg
174         35                  40                  45
176 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala
177     50                  55                  60
179 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro
180 65                  70                  75                  80
182 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala
183                 85                  90                  95
185 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn
186             100                 105                 110
188 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys
189         115                 120                 125
191 Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln
192     130                 135                 140
194 Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser
195 145                 150                 155                 160
197 Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val
198                 165                 170                 175
200 Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala
201             180                 185                 190
203 Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala
204         195                 200                 205
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```
206 Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys
207     210                 215                 220
209 Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys
210 225                 230                 235                 240
212 Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val
213                 245                 250                 255
215 Asn Thr Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile
216             260                 265                 270
218 Val Ala Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala
219         275                 280                 285
221 Gly Ala Ala Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala
222     290                 295                 300
224 Ala Ala Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln
225 305                 310                 315                 320
227 Ala Val Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala
228                 325                 330                 335
230 Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr
231             340                 345                 350
233 Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val
234         355                 360                 365
236 Phe Ala Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser
237     370                 375                 380
239 Lys Val Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly
240 385                 390                 395                 400
242 Val Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln
243                 405                 410                 415
245 Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly
246             420                 425                 430
248 Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp
249         435                 440                 445
251 Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu
252     450                 455                 460
254 Met Thr Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr
255 465                 470                 475                 480
257 Ala Ala Ile Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe
258                 485                 490                 495
261 <210> SEQ ID NO: 3
262 <211> LENGTH: 302
263 <212> TYPE: PRT
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Description of Artificial Sequence: Codon
268       optimised N-terminal section of Chlamydia
269       pneumoniae protein
271 <220> FEATURE:
272 <221> NAME/KEY: UNSURE
273 <222> LOCATION: (1)..(30)
274 <223> OTHER INFORMATION: S-tag and thrombin cleavage site
276 <220> FEATURE:
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277 <223> OTHER INFORMATION: Positions (297)..(302) comprise Histidine tag
279 <400> SEQUENCE: 3
280 Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
281 1 5 10 15
283 Pro Asp Leu Gly Thr Leu Val Pro Arg Gly Ser Ala Ile Ser Asp Pro
284 20 25 30
286 Asp Thr Asn Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys
287 35 40 45
289 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln
290 50 55 60
292 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg
293 65 70 75 80
295 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala
296 85 90 95
298 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro
299 100 105 110
301 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala
302 115 120 125
304 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn
305 130 135 140
307 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys
308 145 150 155 160
310 Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln
311 165 170 175
313 Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser
314 180 185 190
316 Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val
317 195 200 205
319 Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala
320 210 215 220
322 Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala
323 225 230 235 240
325 Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys
326 245 250 255
328 Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys
329 260 265 270
331 Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val
332 275 280 285
334 Asn Thr Val Ala Ala Ala Leu Glu His His His His His His
335 290 295 300
338 <210> SEQ ID NO: 4
339 <211> LENGTH: 9
340 <212> TYPE: PRT
341 <213> ORGANISM: Chlamydia pneumoniae
343 <400> SEQUENCE: 4
344 Ser Ala Lys Leu Glu Thr Pro Glu Leu
345 1 5
348 <210> SEQ ID NO: 5
349 <211> LENGTH: 7

VERIFICATION SUMMARY DATE: 01/14/2002
PATENT APPLICATION: **US/09/889,314** TIME: 13:39:59

Input Set : **A:\1990035b.app**
Output Set: **N:\CRF3\01142002\I889314.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:280 W: Numeric Identifier already exists, <140> found multiple times
L:13 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date